

Amendments to the Specification:

Please amend the specification by inserting the replacement paragraph below at page 1, lines 5-7.

The present application is a National Phase entry of PCT/KR03/00131, filed on January 21, 2003, which claims priority from is based on Korean patent application No. 2002-004297, filed on January 24, 2002, and Korean patent application No. 2002-0011648 filed on March 5, 2002.

Please amend the specification by inserting the replacement paragraph below at page 1, lines 12-15.

The present invention relates to a pair of primers specific to Mycobacterial mycobacterial species, more specifically to a pair of primers that can specifically amplify the hsp 65 gene of mycobacteria, a gene fragment of hsp 65, and an identifying method of Mycobacterial mycobacterial species.

LINE 17 Please amend the specification by inserting the replacement paragraph below at page 1, *1/27/10*
lines 12-15.

The genus Mycobacterium Mycobacterium covers a wide range of organisms including obligate species causing serious human and animal disease such as tuberculosis, bovine tuberculosis, and leprosy; opportunistic pathogens; and saprophytic species found in the natural environment. At present, it is known that about 72 species of the genus mycobacterium Mycobacterium have been reported, of which about 25 species are involved in the human diseases.

Please amend the specification by inserting the replacement paragraph below at page 2, lines 1-12.

Tuberculosis is the largest of the Mycobacterial mycobacterial infections. The Mycobacterial mycobacterial species causing tuberculosis include M. tuberculosis, M. bovis, M.

Mycobacterial diseases other than tuberculosis. *Clin Infect Dis* 15: 1-10, 1992). Accordingly, Myeobacteria mycobacteria need to be differentiated and identified on a species level.

Please amend the specification by inserting the replacement paragraph below at page 3, lines 9-20.

A biochemical method for identifying Myeobacterial mycobacterial species is laborious and time-consuming due to the slow growing rate of Myeobacteria mycobacteria. A cell wall lipid analyzing method using High-performance Lipid Chromatography (HPLC) and Thin Layer Lipid Chromatography (TLC) is difficult to perform and is costly, and thus it is carried out on a small laboratory scale. The use of conventional identifying methods has a disadvantage in that it takes a great deal of time to perform due to the slow growing rate of the Myeobacteria mycobacteria (about 2-3 months for slow-growing mycobacteria). Thus, the treatment of Myeobacterial mycobacterial infection can be delayed (Nolte FS, Metchock B: *Mycobacterium*, In Murray PR, Baron EJ, Pfaller MA, Tenover FC, Yolken RH (eds.), *Manual of clinical microbiology*. American Society for Microbiology, Washington, D.C. 400-437, 1995.).

Please amend the specification by inserting the replacement paragraph below beginning at page 3, line 21 through page 4, line 5.

16s rDNA is commonly used as a chronometer molecule for identification of the Myeobacterial mycobacterial species with a molecular biological method. In 1990, the nucleic acid sequence of 16s rDNA was analyzed, and it shows the phylogenetic relationship of Myeobacteria mycobacteria well. Until now, various methods of identifying Myeobacterial mycobacterial species by using the 16S rDNA have been developed and studied (Comparative sequence analysis, Probe hybridization, and Polymerization chain, reaction-restriction fragment length polymorphism).

Please amend the specification by inserting the replacement paragraph below beginning at page 3, line 6-22.

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